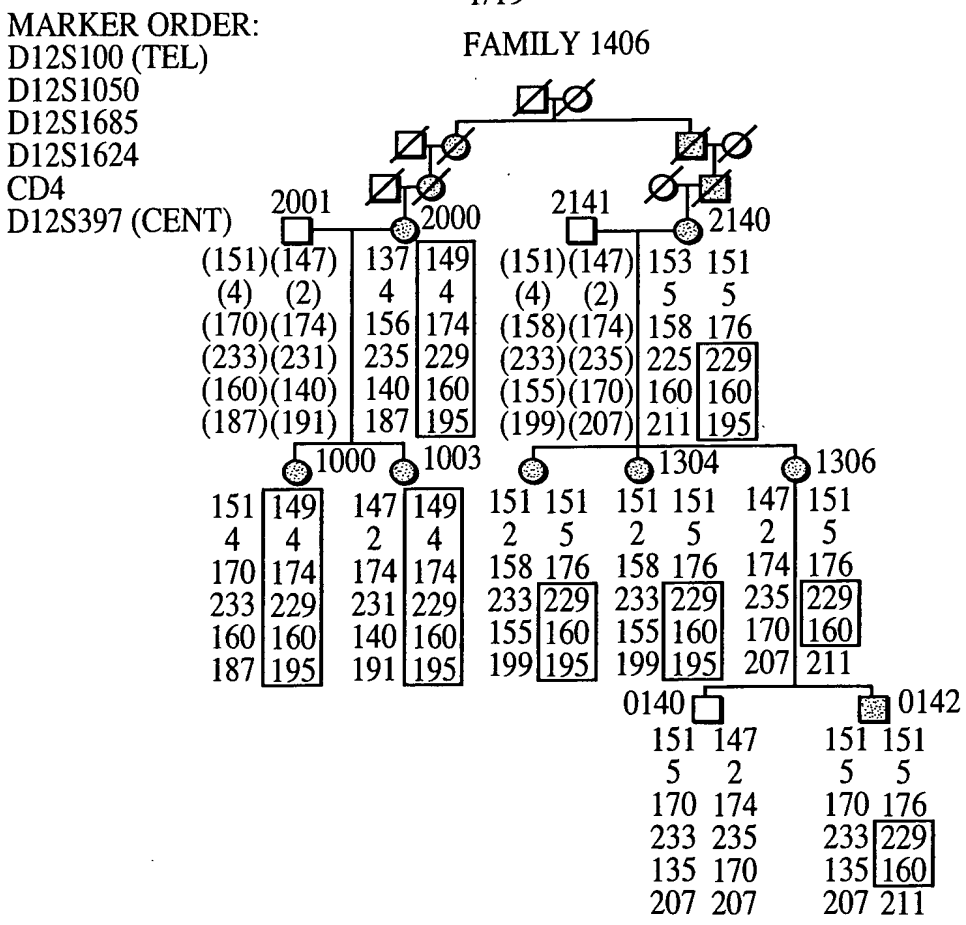
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D12S1050
D12S1685
D12S1624
CD4
D12S397 (CENT)
FAMILY 1406
2001
2000
2141
2140
1000
1003
1304
1306
0140
0142
FAMILY 1478
MARKER ORDER:
D12S100 (TEL)
D12S1050
D12S1685
D12S1624
D12S1594
D12S397 (CENT)
1000
1001
0101
0102
0001
0100
9000

FIG. 1A

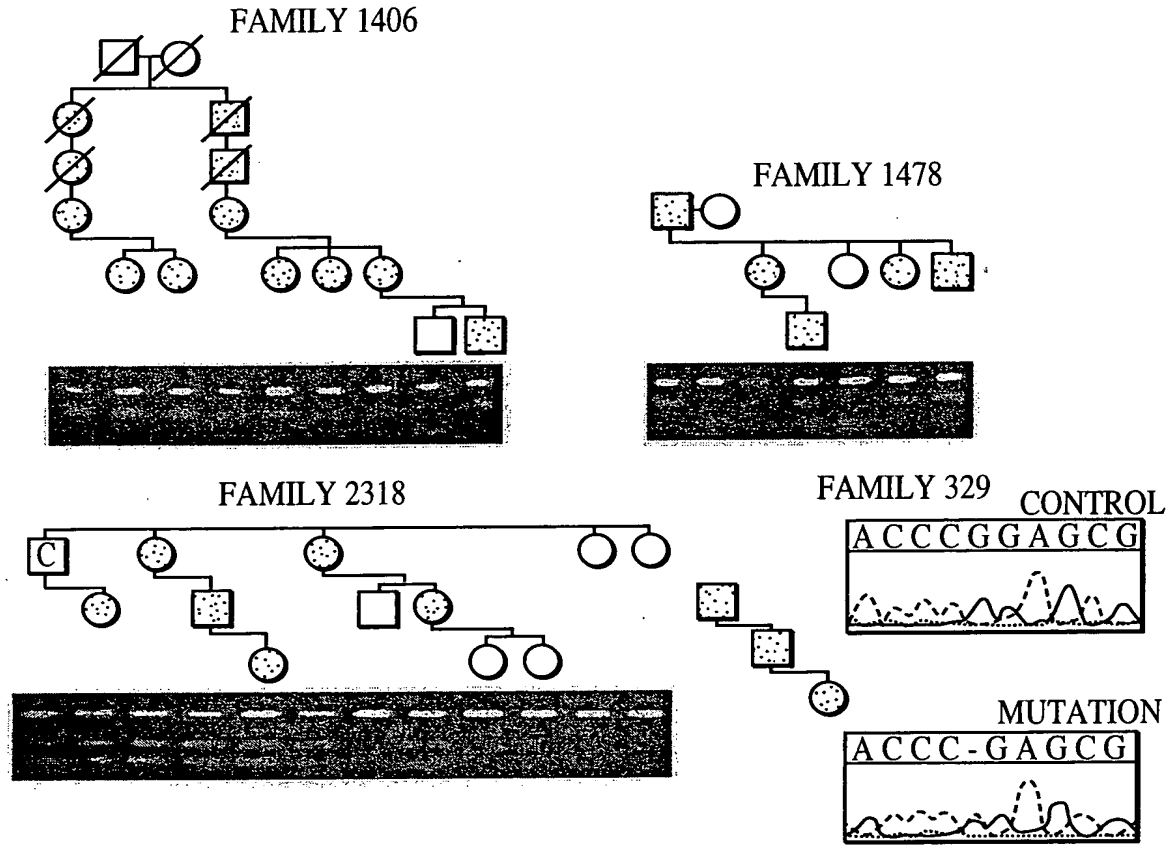

FAMILY 1406
FAMILY 1478
FAMILY 2318
C
FAMILY 329
CONTROL
ACCCGGAGCG
MUTATION
ACCC-GAGCG

FIG. 1B

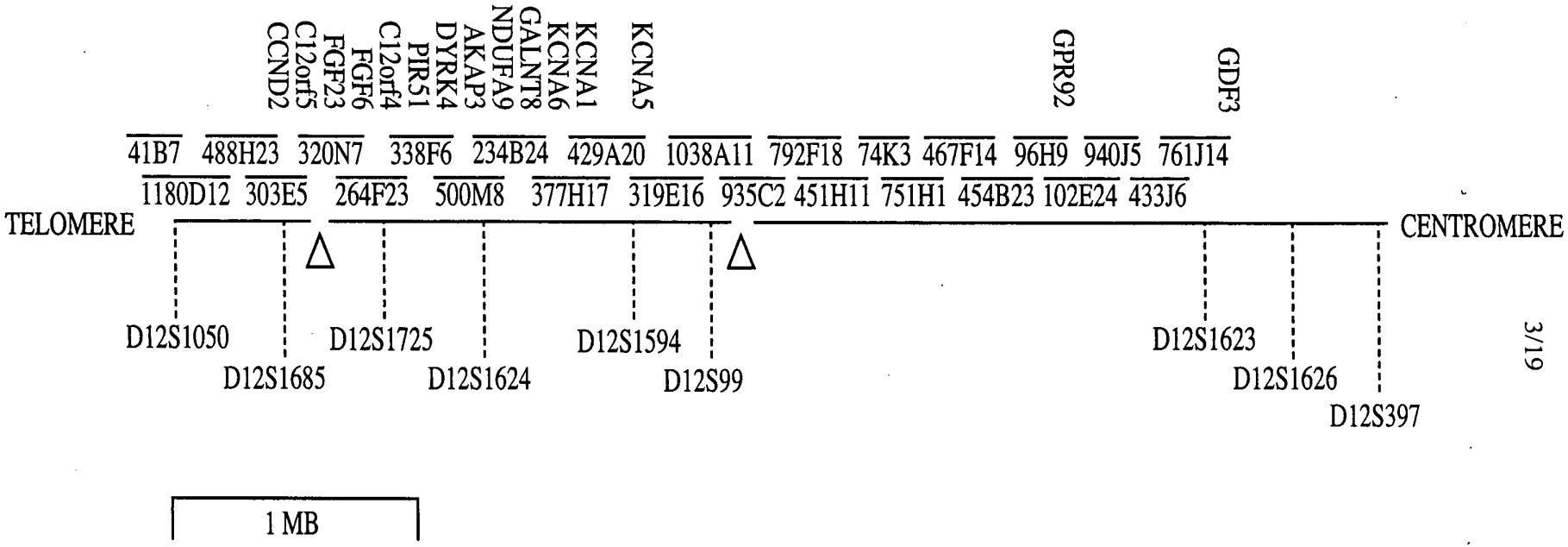


FIG. 2

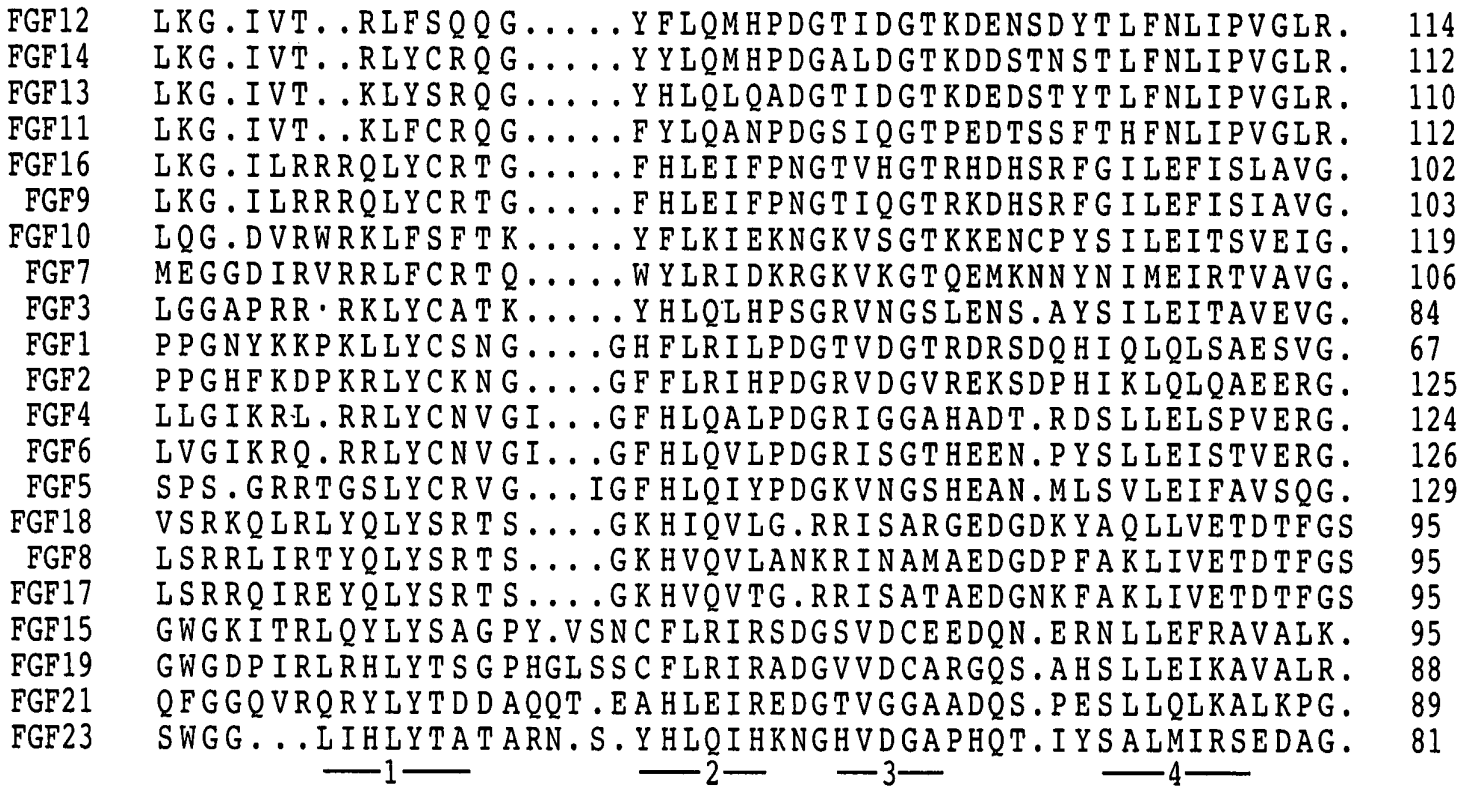


FIG. 3A

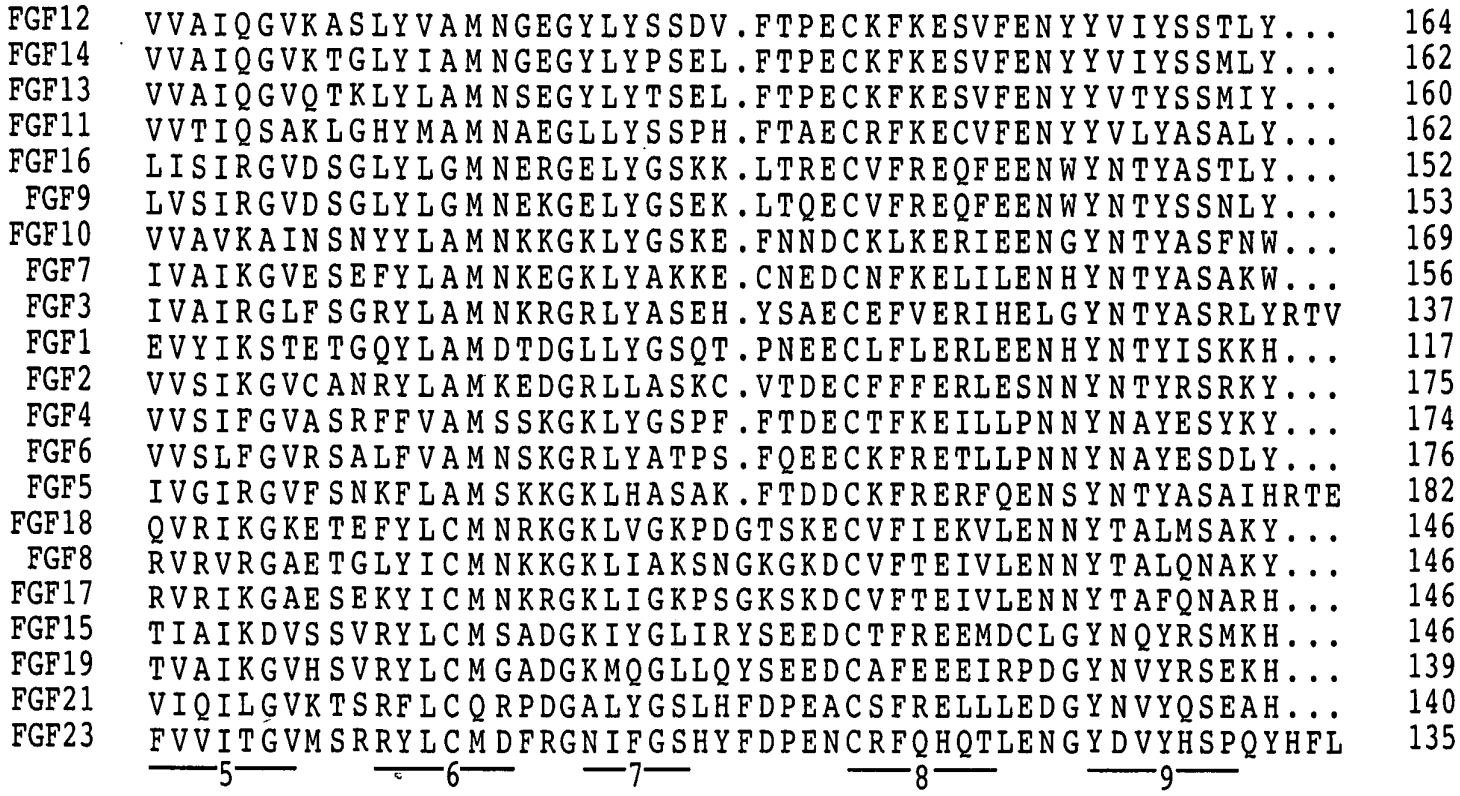
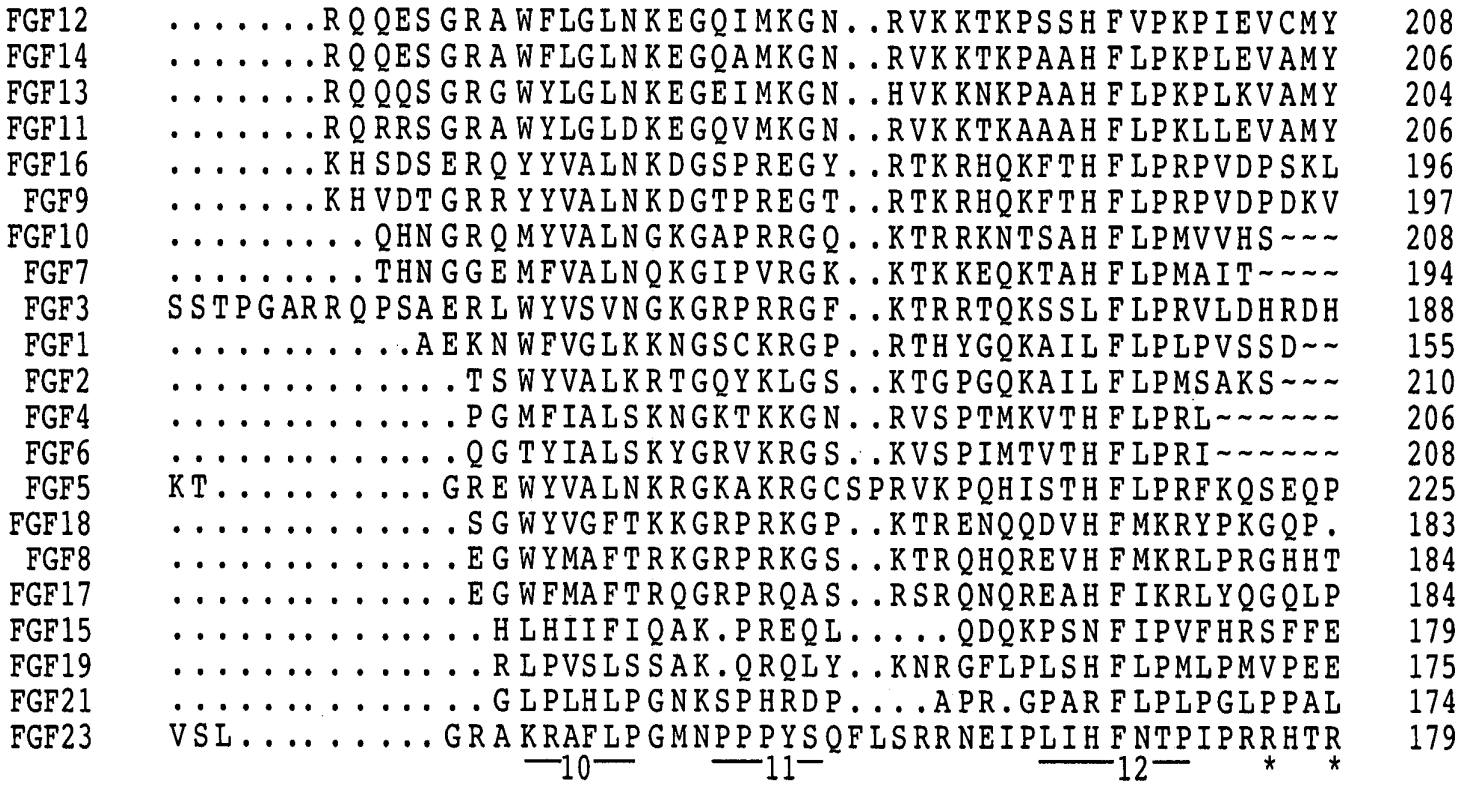

FGF12 VVAIQGVKASLYVAMNGEGYLYSSDV.FTPECKFKESVFENYYVIYSSTLY... 164
FGF14 VVAIQGVKTGLYIAMNGEGYLYPSEL.FTPECKFKESVFENYYVIYSSMLY... 162
FGF13 VVAIQGVQTKLYLAMNSEGYLYTSEL.FTPECKFKESVFENYYVTYSSMIY... 160
FGF11 VVTIQSAKLGHYMAMNAEGLLYSSPH.FTAECRFKECVFENYYVLYASALY... 162
FGF16 LISIRGVDSGLYLGMNERGELYGSKK.LTRECVFREQFEENWYNTYASTLY... 152
FGF9 LVSIRGVDSGLYLGMNEKGELYGSEK.LTQECVFREQFEENWYNTYSSNLY... 153
FGF10 VVAVKAINSNYYLAMNKKGKLYGSKE.FNNDCKLKERIEENGYNTYASFNW... 169
FGF7 IVAIKGVESEFYLAMNKEGKLYAKKE.CNEDCNFKELILENHYNTYASAKW... 156
FGF3 IVAIRGLFSGRYLAMNKRGRLYASEH.YSAECEFVERIHELGYNTYASRLYRTV 137
FGF1 EVYIKSTETGQYLAMDTDGLLYGSQT.PNEECLFLERLEENHYNTYISKKH... 117
FGF2 VVSIKGVCANRYLAMKEDGRLLASKC.VTDECFFFERLESNNYNTYRSRKY... 175
FGF4 VVSIFGVASRFFVAMSSKGKLYGSPF.FTDECTFKEILLPNNYNAYESYKY... 174
FGF6 VVSLFGVRSALFVAMNSKGRLYATPS.FQEECKFRETLLPNNYNAYESDLY... 176
FGF5 IVGIRGVFSNKFLAMSKKGKLHASAK.FTDDCKFRERFQENSYNTYASAIHRTE 182
FGF18 QVRIKGKETEFYLCMNRKGKLVGKPDGTSKECVFIEKVLENNYTALMSAKY... 146
FGF8 RVRVRGAETGLYICMNKKGKLIAKSNGKGKDCVFTEIVLENNYTALQNAKY... 146
FGF17 RVRIKGAESEKYICMNKRGKLIGKPSGKSKDCVFTEIVLENNYTAFQNARH... 146
FGF15 TIAIKDVSSVRYLCMSADGKIYGLIRYSEEDCTFREEMDCLGYNQYRSMKH... 146
FGF19 TVAIKGVHSVRYLCMGADGKMQGLLQYSEEDCAFEEEIRPDGYNVYRSEKH... 139
FGF21 VIQILGVKTSRFLCQRPDGALYGSLHFDPEACSFRELLLEDGYNVYQSEAH... 140
FGF23 FVVITGVMSRRYLCMDFRGNIFGSHYFDPENCRFQHQTLENGYDVYHSPQYHFL 135
5
6
7
8
9

FIG. 3B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FGF14 .....RQQESGRAWFLGLNKEGQAMKGN..RVKKTKPAAHFLPKPLEVAMY 206
FGF13 .....RQQQSGRGWYLGLNKEGEIMKGN..HVKKNKPAAHFLPKPLKVAMY 204
FGF11 .....RQRRSGRAWYLGLDKEGQVMKGN..RVKKTKAAAHFLPKLLEVAMY 206
FGF16 .....KHSDSERQYYVALNKDGSPREGY..RTKRHQKFTHFLPRPVDPSKL 196
FGF9 .....KHVDTGRRYYVALNKDGTPREGT..RTKRHQKFTHFLPRPVDPDKV 197
FGF10 .....QHNGRQMYVALNGKGAPRRGQ..KTRRKNTSAHFLPMVVHS~~~ 208
FGF7 .....THNGGEMFVALNQKGIPVRGK..KTKKEQKTAHFLPMAIT~~~~ 194
FGF3 SSTPGARRQPSAERLWYVSVNGKGRPRRGF..KTRRTQKSSLFLPRVLDHRDH 188
FGF1 .....AEKNWFVGLKKNGSCKRGP..RTHYGQKAILFLPLPVSSD~~ 155
FGF2 .....TSWYVALKRTGQYKLGS..KTGPGQKAILFLPMSAKS~~~ 210
FGF4 .....PGMFIALSKNGKTKKGN..RVSPTMKVTHFLPRL~~~~~~ 206
FGF6 .....QGTYIALSKYGRVKRGS..KVSPIMTVTHFLPRI~~~~~~ 208
FGF5 KT.....GREWYVALNKRGKAKRGCSPRVKPQHISTHFLPRFKQSEQP 225
FGF18 .....SGWYVGFTKKGRPRKGP..KTRENQQDVHFMKRYPKGQP. 183
FGF8 .....EGWYMAFTRKGRPRKGS..KTRQHQREVHFMKRLPRGHHT 184
FGF17 .....EGWFMAFTRQGRPRQAS..RSRQNQREAHFIKRLYQGQLP 184
FGF15 .....HLHIIFIQAK.PREQL.....QDQKPSNFIPVFHRSFFE 179
FGF19 .....RLPVSLSSAK.QRQLY..KNRGFLPLSHFLPMLPMVPEE 175
FGF21 .....GLPLHLPGNKSPHRDP....APR.GPARFLPLPGLPPAL 174
FGF23 VSL.....GRAKRAFLPGMNPPPYSQFLSRRNEIPLIHFNTPIPRRHTR 179
—10— —11— ——12— * *

FIG. 3C

FIG. 4A

FIG. 4B

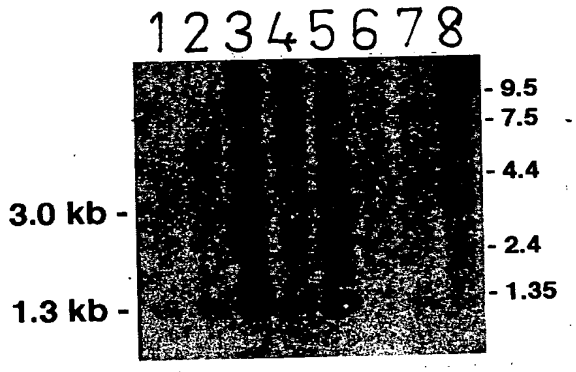

Figure 5A

CGGCAAAAAGGAGGGAATCCAGTCTAGGATCCTCACACCAGCTACTTGC
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GGAGTGTCAGGTTTCAATCTCAGCACCAGCCACTCAGAGCAGGGCACGA
TGTTGGGGGCCCGCCTCAGGCTCTGGGTCTGTGCCTTGTGCAGCGTCTG
CAGCATGAGCGTCCTCAGAGCCTATCCCAATGCCTCCCCACTGCTCGGC
TCCAGCTGGGGTGGCCTGATCCACCTGTACACAGCCACAGCCAGGAACA
GCTACCACCTGCAGATCCACAAGAATGGCCATGTGGATGGCGCACCCCA
TCAGACCATCTACAGTGCCCTGATGATCAGATCAGAGGATGCTGGCTTT
GTGGTGATTACAGGTGTGATGAGCAGAAGATACCTCTGCATGGATTTCA
GAGGCAACATTTTTGGATCACACTATTTCGACCCGGAGAACTGCAGGTT
CCAACACCAGACGCTGGAAAACGGGTACGACGTCTACCACTCTCCTCAG
TATCACTTCCTGGTCAGTCTGGGCCGGGCGAAGAGAGCCTTCCTGCCAG
GCATGAACCCACCCCCGTACTCCCAGTTCCTGTCCCGGAGGAACGAGAT
CCCCCTAATTCACTTCAACACCCCCATACCACGGCGGCACACCCGGAGC
GCCGAGGACGACTCGGAGCGGGACCCCCTGAACGTGCTGAAGCCCCGGG
CCCGGATGACCCCGGCCCCGGCCTCCTGTTCACAGGAGCTCCCGAGCGC
CGAGGACAACAGCCCGATGGCCAGTGACCCATTAGGGGTGGTCAGGGGC
GGTCGAGTGAACACGCACGCTGGGGGAACGGCCCGGAAGGCTGCCGCC
CCTTCGCCAAGTTCATCTAGGGTCGCTGGAAGGGCACCCTCTTTAACCC
ATCCCTCAGCAAACGCAGCTCTTCCCAAGGACCAGGTCCCTTGACGTTC
CGAGGATGGGAAAGGTGACAGGGGCATGTATGGAATTTGCTGCTTCTCT
GGGGTCCCTTCCACAGGAGGTCCTGTGAGAACCAACCTTTGAGGCCCAA
GTCATGGGGTTTCACCGCCTTCCTCACTCCATATAGAACACCTTTCCCA
ATAGGAAACCCCAACAGGTAAACTAGAAATTTCCCCTTCATGAAGGTAG
AGAGAAGGGGTCTCTCCCAACATATTTCTCTTCCTTGTGCCTCTCCTCT
TTATCACTTTTAAGCATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
GCAGTGGGTTCCTGAGCTCAAGACTTTGAAGGTGTAGGGAAGAGGAAAT
CGGAGATCCCAGAAGCTTCTCCACTGCCCTATGCATTTATGTTAGATGC
CCCGATCCCACTGGCATTTGAGTGTGCAAACCTTGACATTAACAGCTGA
ATGGGGCAAGTTGATGAAAACACTACTTTCAAGCCTTCGTTCTTCCTTG
AGCATCTCTGGGGAAGAGCTGTCAAAAGACTGGTGGTAGGCTGGTGAAA
ACTTGACAGCTAGACTTGATGCTTGCTGAAATGAGGCAGGAATCATAAT
AGAAAACTCAGCCTCCCTACAGGGTGAGCACCTTCTGTCTCGCT

Figure 5B

MLGARLRLWVCALCSVCSMSVLRAYPNASPLLGSSWGGLIHLYTATARN
SYHLQIHKNGHVDGAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDF
RGNIFGSHYFDPENCRFQHQTLENGYDVYHSPQYHFLVSLGRAKRAFLP
GMNPPPYSQFLSRRNEIPLIHFNTPIPRRHTRSAEDDSERDPLNVLKPR
ARMTPAPASCSQELPSAEDNSPMASDPLGVVRGGRVNTHAGGTGPEGCR
PFAKFI

Figure 6A

AGCCTGTCTGGGAGTGTCAGATTTCAAACTCAGCATTAGCCACTCAGTG
CTGTGCAATGCTAGGGACCTGCCTTAGACTCCTGGTGGGCGTGCTCTGC
ACTGTCTGCAGCTTGGGCACTGCTAGAGCCTATCCGGACACTTCCCCAT
TGCTTGGCTCCAACTGGGGAAGCCTGACCCACCTGTACACGGCTACAGC
CAGGACCAGCTATCACCTACAGATCCATAGGGATGGTCATGTAGATGGC
ACCCCCCATCAGACCATCTACAGTGCCCTGATGATTACATCAGAGGACG
CCGGCTCTGTGGTGATAACAGGAGCCATGACTCGAAGGTTCCTTTGTAT
GGATCTCCACGGCAACATTTTTGGATCGCTTCACTTCAGCCCAGAGAAT
TGCAAGTTCCGCCAGTGGACGCTGGAGAATGGCTATGACGTCTACTTGT
CGCAGAAGCATCACTACCTGGTGAGCCTGGGCCGCGCCAAGCGCATCTT
CCAGCCGGGCACCAACCCGCCGCCCTTCTCCCAGTTCCTGGCTCGCAGG
AACGAGGTCCCGCTGCTGCATTTCTACACTGTTCGCCCACGGCGCCACA
CGCGCAGCGCCGAGGACCCACCGGAGCGCGACCCACTGAACGTGCTCAA
GCCGCGGCCCCGCGCCACGCCTGTGCCTGTATCCTGCTCTCGCGAGCTG
CCGAGCGCAGAGGAAGGTGGCCCCGCAGCCAGCGATCCTCTGGGGGTGC
TGCGCAGAGGCCGTGGAGATGCTCGCGGGGGCGCGGGAGGCGCGGATAG
GTGTCGCCCCTTTCCCAGGTTCGTCTAGGTCCCCAGGCCAGGCTGCGTC
CGCCTCCATCCTCCAGTCGGTTCAGCCCACGTAGAGGAAGGACTAGGGT
ACCTCGAGGATGTCTGCTTCTCTCCCTTCCCTATGGGCCTGAGAGTCAC
CTGCGAGGTTCCAGCCAGGCACCGCTATTCAGAATTAAGAGCCAACGGT
GGGAGGCTGGAGAGGTGGCGCAGACAGTTCTCAGCACCCACAAATACCT
GTAATTCTAGCTCCAGGGGAATCTGTACTCACACACACACACATCCACA
CACACACACACACACATACATGTAATTTTAAATGTTAATCTGATTTAAA
GACCCCAACAGGTAAACTAGACACGAAGCTCTTTTTATTTTATTTTACT
AACAGGTAAACCAGACACTTGGCCTTTATTAGCCGGGTCTCTTGCCTAG
CATTTTAATCGATCAGTTAGCACGAGGAAAGAGTTCACGCCTTGAACAC
AGGGAAGAGGCCATCTCTGCAGCTTCTAGTTACTATTCTGGGATTCACG
GGTGTTTGAGTTTGAGCACCTTGACCTTAATGTCTTCACTAGGCAAGTC
GAAGAAAGACGCGCATTTCTTCTCTTTGGGAAGAGCTTTGGATTGGCGG
GAGGCTGACAAGGACACCTAAACCGAACACATTTCAGAGTTCAGCCTCC
CTGAGGAATGATTCGCCAATGATTCTGTGATAGGACCAGTCAGTAGCTT
TTGAATTTGCCCTGGCTCAGCAAAGTCTACCTTGCTAGGG

Figure 6B

MLGTCLRLLVGVLCTVCSLGTARAYPDTSPLLGSNWGSLTHLYTATART
SYHLQIHRDGHVDGTPHQTIYSALMITSEDAGSVVITGAMTRRFLCMDL
HGNIFGSLHFSPENCKFRQWTLENGYDVYLSQKHHYLVSLGRAKRIFQP
GTNPPPFSQFLARRNEVPLLHFYTVRPRRHTRSAEDPPERDPLNVLKPR
PRATPVPVSCSRELPSAEEGGPAASDPLGVLRRGRGDARGGAGGADRCR
PFPRFV

FIG. 7A

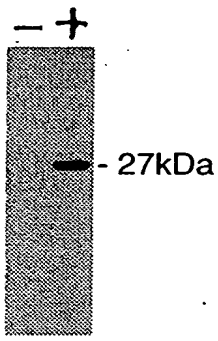


FIG. 7B

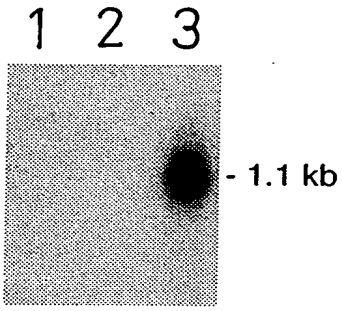


FIG. 7C

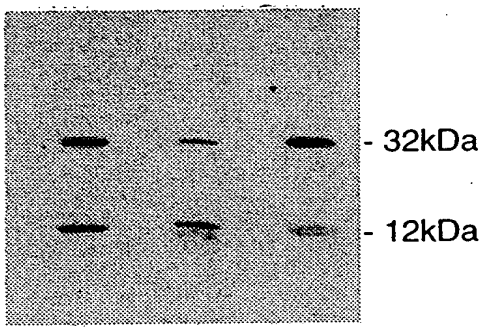


FIG. 8A

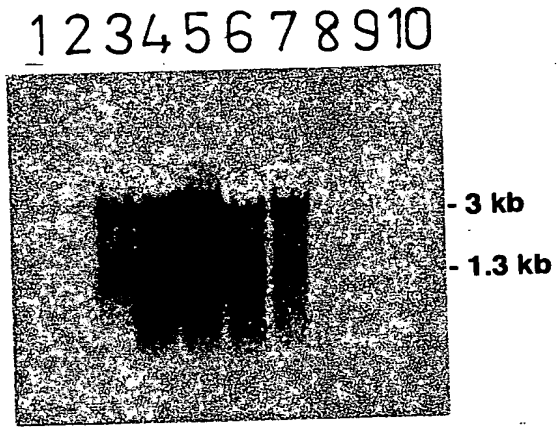


FIG. 8B

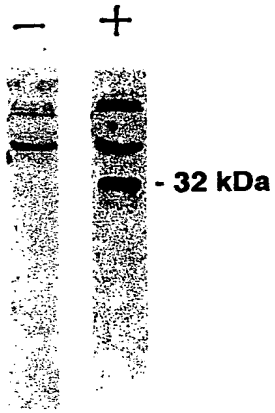
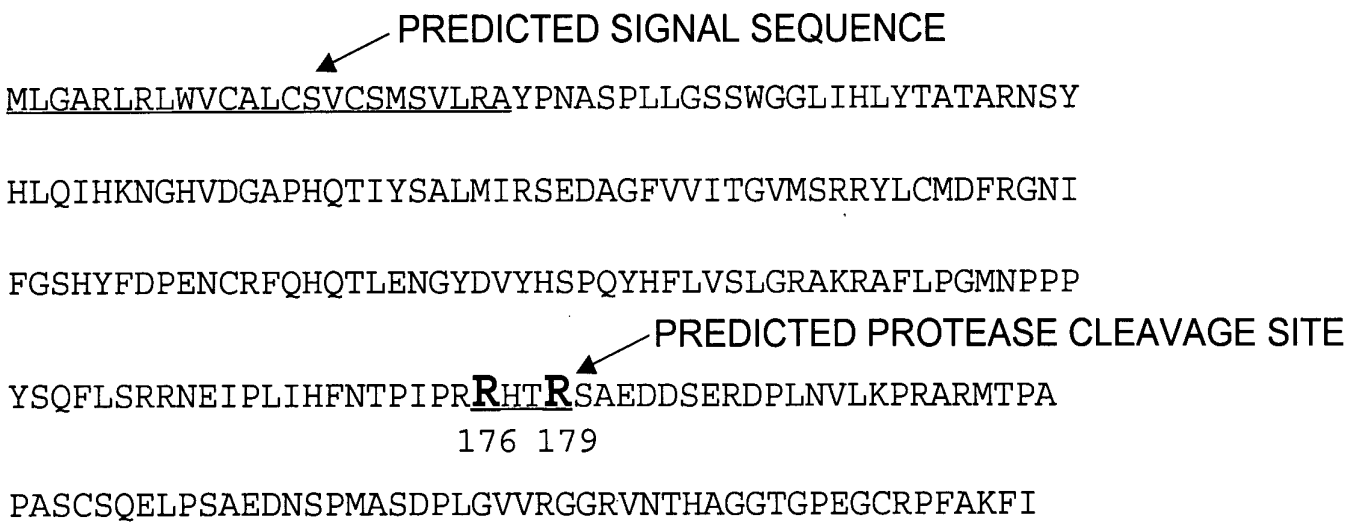


Figure 9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HLQIHKNGHVDGAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNI
FGSHYFDPENCRFQHQTLENGYDVYHSPQYHFLVSLGRAKRAFLPGMNPPP
PREDICTED PROTEASE CLEAVAGE SITE
YSQFLSRRNEIPLIHFNTPIPRRHTRSAEDDSERDPLNVLKPRARMTPA
176 179
PASCSQELPSAEDNSPMASDPLGVVRGGRVNTHAGGTGPEGCRPFAKFI

FIG. 10A

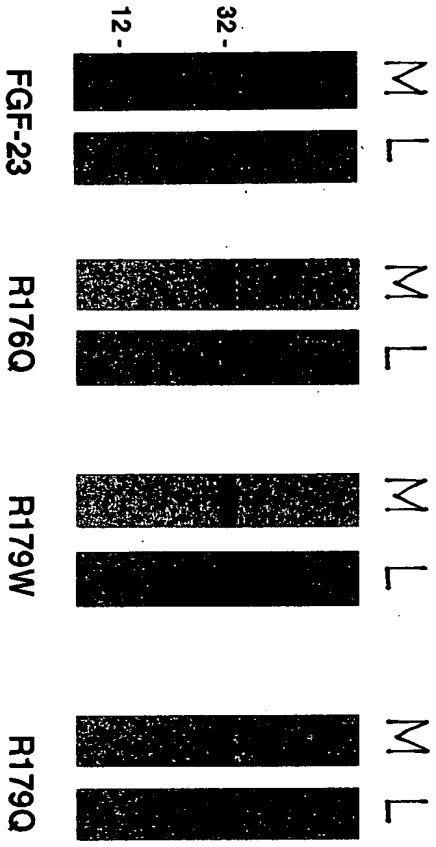

Figure 10B

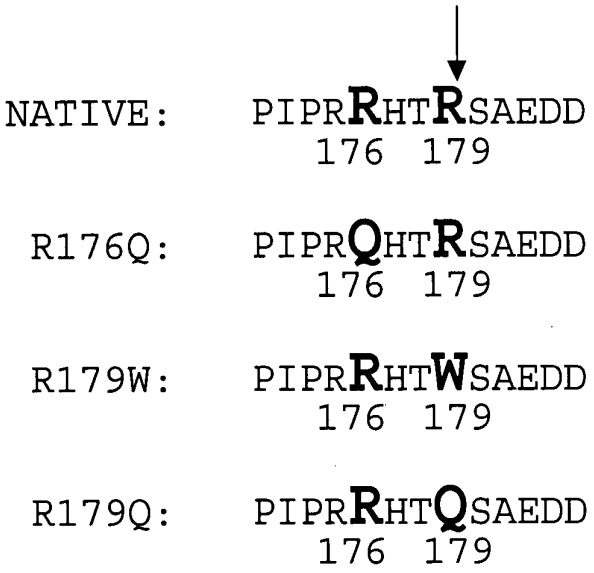
NATIVE: PIPRRHTRSAEDD
176 179
R176Q: PIPRQHTRSAEDD
176 179
R179W: PIPRRHTWSAEDD
176 179
R179Q: PIPRRHTQSAEDD
176 179

FIG. 11A

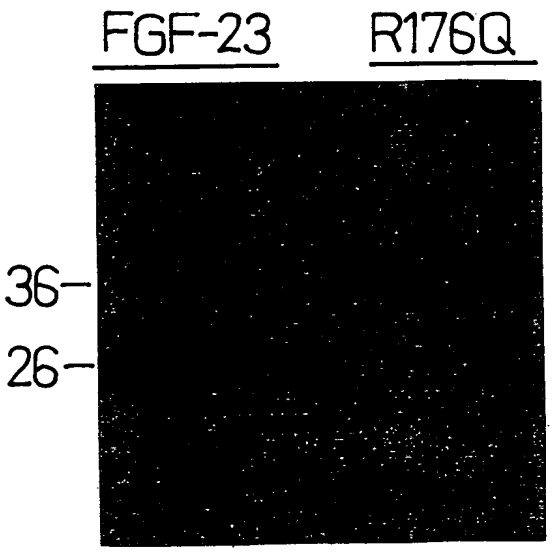

FIG. 11B

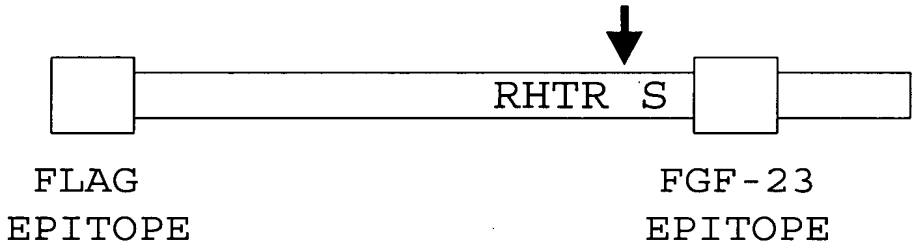

FIG. 12A

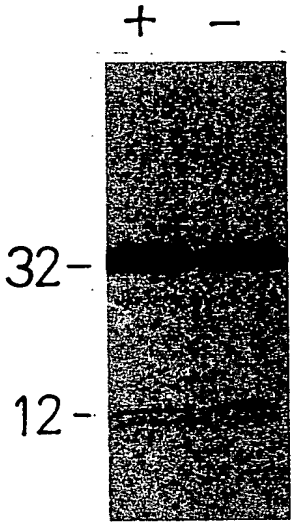

FIG. 12B

FIG. 13